



08/984079

20 40
CTT TCT ATT TGG TTA ACC ATG GCT CAT AAC TTT CGT CAT CCT TTC TTC
Leu Ser Ile Trp Leu Thr Met Ala His Asn Phe Arg His Pro Phe Phe>
60 80
CTT TTC CAA CTT TTA CTC ATT ACT GTC TCA CTA ATG ATC GGT AGC CAC
Leu Phe Gln Leu Leu Ile Thr Val Ser Leu Met Ile Gly Ser His>
100 120 140
ACC GTC TCG TCA GCG GCT CGA CAT TTA TTC CAC ACA CAA ACA ACC TCA
Thr Val Ser Ser Ala Ala Arg His Leu Phe His Thr Gln Thr Thr Ser>
160 180
TCA GAG CTG CCA CAA TTG GCT TCA AAA TAC GAA AAG CAC GAA GAG TCT
Ser Glu Leu Pro Gln Leu Ala Ser Lys Tyr Glu Lys His Glu Glu Ser>
200 220 240
GAA TAC AAA CAG CCA AAA TAT CAT GAA GAG TAC CCA AAA CAT GAG AAG
Glu Tyr Lys Lys Gln Pro Lys Tyr His Glu Glu Tyr Pro Lys His Glu Lys>
260 280
CCT GAA ATG TAC AAG GAG GAA AAA CAA AAA CCC TGC AAA CAT CAT GAA
Pro Glu Met Tyr Lys Glu Glu Lys Lys Gln Lys Pro Cys Lys His His Glu>
300 320
GAG TAC CAC GAG TCA CGC GAA TCG AAG GAG CAC GAA GAG TAC GAT AAA
Glu Tyr His Glu Ser Arg Glu Ser Lys Glu His Glu Glu Tyr Asp Lys>

FIGURE 1A



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340
GAA AAA CCC GAT TTC CCC AAA TGG GAA AAG CCT AAA GAG CAC GAG AAA
Glu Lys Pro Asp Phe Pro Lys Trp Glu Lys Pro Lys Glu His Glu Lys>
360
400
CAC GAA GTC GAA TAT CCG AAA ATA CCC GAG TAC AAG GAC AAA CAA GAT
His Glu Val Glu Tyr Pro Lys Ile Pro Glu Tyr Lys Asp Lys Gln Asp>
420
440
GAG AAT AAG AAA CAT AAA GAT GAA GAG TGC CAG GAG TCA CAC GAA TCG
Glu Asn Lys Lys His Lys Asp Glu Glu Cys Gln Glu Ser His Glu Ser>
460
480
500
AAA GAG CAC GAA GAG TAC GAG AAA GAA AAA CCC GAT TTC CCC AAA TGG
Lys Glu His Glu Glu Tyr Glu Lys Glu Lys Pro Asp Phe Pro Lys Trp>
520
540
GAA AAG CCT AAA GGG CAC GAG AAA CAT AAA GCC GAA TAT CCG AAA ATA
Glu Lys Pro Lys Glu His Glu Lys His Lys Ala Glu Tyr Pro Lys Ile>
560
580
CCT GAG TGC AAG GAA AAA CTA GAT GAG GAT AAG GAA CAT AAA CAT GAG
Pro Glu Cys Lys Glu Lys Leu Asp Glu Asp Lys Glu His Lys His Glu>
600
620
640
TTC CCA AAG CAT GAA AAA GAA GAG GAG AAG AAA CCT GAG AAA GGC ATA
Phe Pro Lys His Glu Lys Glu Glu Lys Lys Pro Glu Lys Gly Ile>
660

FIGURE 1B



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680 720
GTA CCC TGA GTG GGT TAA AAT GCC TGA ATG GCC GAA GTC CAT GTT TAC
Val Pro *** Val Gly *** Asn Ala *** Met Ala Glu Val His Val Tyr>
740 760
TCA GTC TGG CTC GAG CAC TAA GCC TTA AGC CAT ATG ACA CTG GTG CAT
Ser Val Trp Leu Glu His *** Ala Leu Ser His Met Thr Leu Val His>
780 800 *
GTG CCA TCA TCA TGC AGT AAT TTC ATG GGA TAT TGT AAT TAT ATT GTT
Val Pro Ser Ser Cys Ser Asn Phe Met Gly Tyr Cys Asn Tyr Ile Val>
820 840 860
AAT AAA AAA GAT GGT GAG TGG GAA ATG TGT GTG TGC ATT CAT CCA TGA
Asn Lys Lys Asp Gly Glu Trp Glu Met Cys Val Cys Ile His Pro ***>
880 900 *
GCA ATG CTG AAT CTC TTT GCA TGC ATA GAG ATT CTG AAT GGT TAT AGT
Ala Met Leu Asn Leu Phe Ala Cys Ile Glu Ile Leu Asn Gly Tyr Ser>
920 940 960
TTA TGT TAT ATC GTT TGT TCT AGT GAA ATT AAT TTT GAA TGT TGT ATG
Leu Cys Tyr Ile Val Cys Ser Ser Glu Ile Asn Phe Glu Cys Cys Met>
TAA TGT T
*** Cys Xxx>

FIGURE 1C



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20 60
ACTAAAGGA ACAAAAGCTG GAGCTCCACC GCGGTGGCG CCGCTCTAGA ACTAGTGGAT
40
80 120
CCCCCGTGGA CTAAACAAAA CATGGGAAGA TTTGCTGTAA AAAAAATAAA GAAGCTTACT
100 *
140 180
CAATAACACT TTGTGAATTG TATACAAAAG ACTCAATGAA AAACAATAAC TCAATACACT
160
200 240
TTTTTTCAC TATTACATC CTTTATATAG GCTGAAACTA CAACAACCTT AGCTAAAAAA
260 300 *
ATAGGATAAC CTAATAGCAA AATCACAATC AGATATTAA CCAATGATTT AGCTAACCAT
320 360
TTAACAACTT TATTGAAACT AATTGAATA TTTCATCTGC TGATATGCCC AAGATTTTAG
340
380 420
GCCACTAACC GATTGTGTGG TGAACCTTAA CATGTCATGC ATTTGTAACT GTTTGAAACA
400 *
440 480
AGTTTTTTGC ATTATTTTAC TATATGAACT GTTTGATTAG GTTGAGTTAC AACTGAGCT
460
500 540
TGTAAGCTCA CTCAAAATTT TCTAATTCT AAGTGATCA GCAAACTAG GACCGGCGG
520 *
560 600 *
CGTACGAGAG CTCGGATTGA TTTTCTAGTT AATAAATAAG ACGATTATG TTTTAAACT

Figure 2A



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620	ATTATGGACT TTTTGGACTA TGTAAGTGT	640	TTTGTGTTTT TTATTTGCTT	660
680	TTTTTGGATT TAGTAATTAT TATTTTTAAA	700	CTGCAAAATT ATATGTTTTT	720
740	TCACAGTTTT CAAAATTCCA TAACTTAGAA	760	TTTTTCGCTG CAAAATAAAG	780
800	AGTGTTTTTT CTGTAATAAA ATAAATAAAT	820	AGTATTTTCC TAAAAATTGG	840
860	AAATTGATTT ACCAAAATTA GTATGTCAAA	880	ACACATGTTT ATATGTTACA	900
920	GTCTAGGCAA ATAACATCTA GCGGGGGTTT	940	AGGGCGAGTG GGCTCATTTT	960
980	GAGTAAGTAT AGTTAGGGCC GAGTTTTAGA	1000	TTGCAATATC AAGGTCAAAG	1020
1040	CTTCGATGAA TGATATGTAT GATTGTCCGA	1060	TTAACGAAAT ATGTTTTTTT	1080
1100	TGTTTTATCT CGTGTGATAA GTATATAGTA	1120	TGTTTTATC CAATCTTAT	1140
1160	ATTGTGGCTA TTCTAAATTA ATTGATTTGT	1180	TATTATTGAA ATCTGATGCA	1200

Figure 2B



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1220	AAAGCATGGA	ATCTCATGCC	TACTGCTTTC	TGTTAAGAT	1240	ACGATTGCAA	GTTTAAACATG	1260
1280	CTTACTATTT	TGATTTTGTC	CTTGCAATGCT	ATGTCACATT	1300	ACATGGGGTT	GGGATGATAT	1320
1340	GGTAAGGAGG	AAGTTTGTGAC	AGTTTAAATGA	TTTGCACTAT	1360	CTGGTGGTTT	AACCACATAT	1380
1400	TTGTTATGGC	ATCTTGACTG	CGGTTATGGT	GGCTCGACCG	1420	CCCATATCTG	TTCTGGAAAT	1440
1460	TTATCTGTGA	CTCTGGTGGC	ATTGTCTACA	ATTATTTGTT	1480	GGTGTGTTTT	GGATGGACGA	1500
1520	GTCGTGGGGA	ACTCTATTTG	GTGTGTTGCC	GAGTTGGGTA	1540	GGAAATTTTC	GAAAAAAATT	1560
1580	TGCATTGTGT	TTTTTCTGAAA	AATATTGCAT	TAAACATAATC	1600	ATGCATTCTC	AATTTTGGTC	1620
1640	AATTGAACGT	TATAAAAATTC	TCTATGATAT	CCTGATCTGT	1660	TTATTACATT	ATATGTGTTT	1680
1700	ATGCTTGAGT	TAAGTCAAAC	ATTGAGATTC	ATAGCTCACC	1720	CAATTATTTA	ATCATTTCAG	1740
1760	GCAATCTGCA	GACTTAGGAT	TGGATGGCGT	TCAGGAGCTT	1780	GGATTGGTTT	TCTCACATCA	1800
1820	TATTTTATTA	AATAATTATT	AATTAAAAAT	TATGGACTTT	1840	TGGACTGTCT	GACTAAATTTT	1860

Figure 2C

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20 40 60
ACTAAAGGGA ACAAAGCTG GAGCTCCACC GCGTGGCGG CCGCTCTAGG ATCCCCCGTG
80 100 120
GACTAAACAA AACATGGGAA GATTGCTGT AAAAAAATAA AAGAAGCTTA CTCAATAACA
140 160 180
CTTTGTGAAT TGTATACAAA AGACTCAATG AAAACAATA ACTCAATACA CTTTTTTTCA
200 220 240
CTGATTTACA TCCTTTATAT AGGCTGAAAC TACAACAACT TTAGCTAAAA AAATAGGATA
260 280 300
ACCTAATAGC AAAATCACAA TCAGATATTA AACCATGATT TTAGCTAACC ATTTAACAA
320 340 360
TTTTATTGAAA CTAATTTGAA TATTTCATCT GCTGATATGC CCAAGATTTT AGGCCACTAA
380 400 420
CCGATTGGT GGTGAACTTT AACATGTCTAT GCATTTGTAA CTGTTTGAAA CAAGTTTTTT
440 460 480
GCATTATTTT ACTATAATGAA CTGTTTGATT AGGTTGAGTT ACACACTGAG CTTGTAAGCT
500 520 540
CACTCAAATT TTTCTAATTT CTAAGGTGAT CAGCAAACTT AGGACCGGGC GGCGTACGAG

Figure 3A



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560 580 600
AGCTCGGATT GATTTTCTAG TTAATAAATA AGACGATTTA TGTTTTAAAA CTATTATGGA *
620 640 660
CTTTTGGAC TATGTAACTG TTTGGGACTT TATTTTGTG TTTTATTGCG TTTTTTTGGG
680 700 720
TTTAGTAATT ATTATTTTAA AACTGCAAAA TTATATGTTT TTACAAACTA AGTCACAGTT
740 760 780
TTCAAAAATC CATAACTTAG AATTTTTCGC TGC AAAATAA AGTAATCATT TAAGTGTTTT
800 820 840
TTCTGTAATA AAATAAATAA ATAATTTTAA CGAGTATTTT CCTAAAAATT GGAAATTGAT
860 880 900
TTACCAAAAT TAGTATGTCA AAACACATGT TTATATGTTA CAGGGCGATA TCGTCTAGGC *
920 940 960
AAATAACATC TAGGCGGGGT TTGGAGTGTT ACAGGGCGAG TGGGCTCATT TTGAGTAAGT
980 1000 1020
ATAGTTAGG CCGAGTTTAA GATTGCATAT TCAAGGTCAA AGATTTTGTA AACTTCGATG *
1040 1060 1080
AATGATATGT ATGATTGTCC GATTAAACGAA ATATGTTTTT TTCTTTTG TGTTGTTTTAT

Figure 3B



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1100	1120	1140
CTCGTGTGAT AAGTATATAG TATGTTTTAT TCCAATTCTT ATGGCATGTG ACATTGTGGC		
1160	1180	1200 *
TATTCTAAAT AAATTGATTT GTTATTATTG AAATCTGATG CATCTGTTCT ACAAAGCATG		
1220	1240	1260
GAATCTCATG CCTACTGCCT TCTGTTAAAG ATACGATTGC AAGTTTAACA TGCTTACTAT		
1280	1300 *	1320
TTTGATTTTG TCCTTGCATG CTATGTCACA TTACATGGGG TTGGGATGAT ATGGTAAGGA		
1340	1360	1380
GGAAAGTTTG ACAGTTTAAT GATTTGCACT ATCTGGTGGT TTAACCACAT ATTTGTTATG		
1400 *	1420	1440
GCATCTTGAC TCGGGTTATG GTGGCTCGAC CGCCCATATC TGTCTCGAA ATTTATCTGT		
1460	1480	1500 *
GACTCTGGTG GCATTGTCTA CAATTATTG TTGGTGTGTT TTGGATGGAC GAGTCGTGGG		
1520	1540	1560
GAACTCTATT TGGTGTGTTG CGGAGTTGGG TAGGAAATTT TCGAAAAAAA TTTCATTTGT		
1580	1600 *	1620
GTTTTCTGA AAAATATTGC ATTAACATAA TCATGCATTC TCAATTTTGG TCAATTGAAC		

Figure 3C



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1640	1660	1680
GTATATAAAAT TCTCTATGAT ATCCTGATCT GTTTATTACA TTATATGTGT TTATGCTTGA		
1700 *	1720	1740
GTAAAGTCAA ACATTGAGAT TCATAGCTCA CCAATTATT TAATCATTTT AGGCAATCTG		
1760	1780	1800 *
CAGACTTAGG ATTGGATGGC GTTCAGGAGC TTGGATTGGT TTTCTCACAT CATATTTTAT		
1820	1840	1860
TAAATAAATTA TTAATTAAAA TTTATGGACT TTTGGACTGT CTGACTAATT TTCAGAAATTT		
1880	1900 *	1920
TATTTTGGTT TTGGGTTTTG TTGAATTTTT TAGATAAATTA TTTTAAATAT TCTGCATAAT		
1940	1960	1980
TTTTCTGTTA TTTGAAAAGG ATGTTTCAAT TTTTTTTCAA AATTGAAAACG TTAAAGAATT		
2000 *	2020	2040
TTTACTACTG CAAATTCAGA ATAAAGTGAAT TTGTTTTTTA GAAAGATTAA ATAAGTTAGT		
2060	2080	2100 *
ATTACGATTT TTAGTTTGAT TTGGTGGAAG GTAATGTATG TTTTGAACA TAATTATTTG		
2120	2140	2160
ACAATAATTA AGTTTCTAG GGAATAAACG GAAATATCTT CTTCTTTTTT GTAAAAATTAC		

Figure 3D



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2180	2200 *	2220
TAATGCAAGA ACAAACAACG TTTTGGGGAG CAAATAATCT AGCTTTAAGT AGTCAGTGTA		
2240	2260	2280
ACTCTCAAAA TCTGGTCATA ACTTCTAGGC TGAGTTTGCT GTGCTACAGT AGTAAAGTCTA		
2300 *	2320	2340
TAGAAACTTA CCTGACAAAA CGACATGACG TCAGGGTCGA ATCTACAACT TTTCCCTTTT		
2360	2380	2400 *
CTTCAATTAA CATATGGTTG ATTCAAGTTC CGATCTATAA TAAATTATTA CGATTTATCA		
2420	2440	2460
ATTCAATTA CCTTATATCA TCCTATTATA AATATAAGTC AGTTCAATTC AGTTTTCGAA		
2480	2500 *	2520
AGTTCCCCAA AATTTTGAAT TTTATTAAAT TTATTCCCTA AAACCGAAAT AGTTATATCT		
2540	2560	2580
TTCAAAATTA AGTTTCATTT TTCAATCCGA TTTCAATTTC ATCCTTTTAT AACTCTCTAT		
2600 *	2620	2640
TATCTATAAT TACATAAATT TCAAAATTAAT TTTGAAATAT TTACACTTTA GTCCCTAAGT		
2660	2680	2700 *
TCAAAACTAT AAATTTTCAC TTTAGAAATT AATCATTTTT CACATCTAAG CATCAAAATTT		

Figure 3E

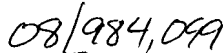


Figure 3F



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3260	3280	3300 *
TGTTATTTAG ATTCTTAAATA TTTTGGAGCA TTCCATACTA TAAATTTCGTA ACATAAATATT		
3320	3340	3360
AAAATATAGT AATATAAAGT GTAATTAACT TTAAATTACA AGCATAAATAT TAAATTTTGA		
3380	3400 *	3420
ATCAATTAAT TTTTATTCTTCT ATTATTTTAA TTAAATTAGT CTATTTTTC AAAATAAAAT		
3440	3460	3480
TTAAATCTAA ATAAAAATAA TTTTTCCTTA ATGTTGAAAC AACTCATGTT ATACTTCAAA		
3500 *	3520	3540
ATTATAAGTA TTATATTTTAC CTTGATGATT TATTTATTAG TATATTAAAT CTGATTATAA		
3560	3580	3600 *
TTATGGTGGG ATACAAATCGC TTTCCACTAA ATATTTTAACT TATGATTAT AAATTTATTT		
3620	3640	3660
CAACATCGTA TATTTACTTA TTAATACATA ATTTATCATA ATTTTATGGA AATTGAGACC		
3680	3700 *	3720
AAGAAACATT AAGAGAACAA ATTCTATAAC AAAGACAATT TAGAAAAAAA TGTACTTTTA		
3740	3760	3780
GGTAATTTTA AGTACTCTTA ACCAAACACA AAAATTCAAA TCAAAATGAAC TAAATAAGAT		

Figure 3G



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3800 * 3820 3840
AATATAACAT ACGGAACATC TTACTTGTA TCTTACATTC CCATAATTTT ATTATGAAAA
3860 3880 3900 *
ATAATCTTAT ATTACTCGAA CTAAATGTTG TCACAAATTA TTATCTAAAT AAAGAAAAAC
3920 3940 3960
ACTTAATTTT TATAACATTT TTTTCATATAT TTGAAGATT ATATTTTGTA TATTTACGTA
3980 4000 * 4020
AAAAATATTG ACATAGATTG AGCACCTTCT TAACATAATC CCACCATAAG TCAAGTATGT
4040 4060 4080
AGATGAGAAA TTGGTACAAA CAACGTGGG CCAAAATCCCA CCAAACCATC TCTCATTTCTC
4100 * 4120
TCCTATAAAA GGCTTGCTAC ACATAGACAA CAATCCACAC A CA AAT ACA CGT TCT
4140 4160 4180
TTT CTT TCT ATT TGA TTA ACC ATG G CTCATAGCAT TCGTCACCCCT TTCTTCCTTT
<Lys Lys Arg Asn Ser *** Gly His
4200 * 4220 4240
TCCAACTTTT ACTCATAAGT GTCTCACTAG TGACCGGTAG CCACACTGTT TCGGCAGCGG
4260 4280 4300 *
CTCGACGTTT ATTCGAGACA CAAGCAACCT CATCAGAGCT CCCACAATTG GCTTCAAAAT

Figure 3H



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4320	ACGAAAAGCA	CGAAGAGTCT	GAATACGAAA	AGCCAGAAATA	CAAACAGCCA	AAGTATCAGG
			4340		4360	
4380			4400		4420	
			*			
AAGAGTACTC	AAAACCTTGAG	AAGCCTGAAA	TGCAAAAGGA	GGAAAAACAA	AAACCCCTGCA	
			4460		4480	
4440						
AACAGCATGA	AGAGTACCAC	GAGTCACACG	AATCAAAGGA	GCAAAAAGAG	TACGAGAAAAG	
			4520		4540	
4500			*			
AAAAATCTCGA	CGGGCCCGAA	GATCTTCGCT	AGCCGTCGAC	GCCCCGGGGA	ATTCTGTCGAG	
			4580		4600	
4560			*			
CCTTGAATCA	TATGACGCTG	GTGCATGTGC	CATCATCATG	CAGTAATTTC	ATGGTATATC	
			4640		4660	
4620						
GTAATATATA	GTAAATAAAA	AAGATGGTGA	TTGGGAAATG	TGTGTGTGCA	TTCTCTCCATG	
			4700		4720	
4680			*			
CACTAATGGT	GAATCTCTTT	GCATACATAG	AAATTCTAAA	TGGTTATAGT	TTATGTTATA	
			4760		4780	
4740						
GTGTATGTTG	TAGTGAAAKT	AATTTTAAAT	GTTGTATCTA	ATGTTAAACAT	CAC TTGGCTT	
			4820		4840	
4800			*			
GATTTATGTT	ATGTTATGTA	TTTTACTTTA	ATGATATTGC	ATGTATTGTT	AATTTAACAT	
			4880		4900	
4860			*			
TGCTTGATCA	TTATACTCTT	CTACTATTAA	TTATAAATGG	CAC TGTGTTTG	TTTAAACTTT	

Figure 3I



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4920		4940	4960		
TTACAAAGTTA	AGACATGTAT	AAATATATGA	CAATATAAAT	ACAAAGTTTTA	GTTCAAATGTT
4980		5000	5020		
AGCTATCTTA	GTAATGTTATT	GATGATCTTA	ATTACATTTA	AACAAATTCC	ACTTAAAAAT
5040		5060	5080		
TTAAATAAATA	ATAACAAATA	ATTATTGTAA	TATAATACAT	TAAATGCAAC	AAAAAATGAA
5100	*	5120	5140		
ATAAATAAAA	TAAATATAGCA	AATAATTGTT	ATAATATTGT	AATATAATAT	GTACCATATT
5160		5180	5200		
CTTAACTGAA	ATAGGGTCTA	ACCTATAATC	CCTAAAAATT	CAGTTTAAAT	ATTTTTATAC
5220		5240	5260		
CTGCCATATT	ATTAGAACTC	TTTTTTAAATA	TATTAAAAAT	TTAATTATAC	CAATTTAATT
5280		5300	5320		
TAAACTATTA	ATTATCTTAA	CTAAAAATCTA	AAATTTTATT	TAACCTATTA	ATTAATTTCC
5340		5360	5380		
TAATTATCTT	ATCTAATTTA	AAACTCTAAT	TATCCTAATT	TGATTTAAAT	TCTTGATAT
5400	*	5420	5440		
CTTAATTTGT	AACCTCCTCC	ACCCAGCTAG	ATGCTGGACC	CGAATCCGGG	AGATTACATC

Figure 3J



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5460 5480 5500 *
GGCATTGAGA TGGCCTAGTA GTGATCAGGG TTTTCTAGAG GTACCCAATT CGCCCTATAG

TGAGTCGT



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AAAAAACA ATG AGC ACT GCA AGA TTT ATC AAG TGT GTC ACG GTC GGT GAT 50
Met Ser Thr Ala Arg Phe Ile Lys Cys Val Thr Val Gly Asp
1 5 10

GGA GCT GTG GGG AAA ACT TGT ATG CTC ATT TCA TAT ACC AGC AAT ACT 98
Gly Ala Val Gly Lys Thr Cys Met Leu Ile Ser Tyr Thr Ser Asn Thr
15 20 25 30

TTC CCA ACG GAT TAT GTT CCA ACA GTA TTT GAT AAC TTT AGT GCC AAT 146
Phe Pro Thr Asp Tyr Val Pro Thr Val Phe Asp Asn Phe Ser Ala Asn
35 40 45

GTG GTG GTG GAT GGC AGC ACA GTG AAC CTT GGC CTA TGG GAC ACT GCC 194
Val Val Val Asp Gly Ser Thr Val Asn Leu Gly Leu Trp Asp Thr Ala
50 55 60

GGG CAA GAA GAT TAT AAT AGG CTA AGG CCA CTG AGT TAT AGA GGA GCT 242
Gly Gln Glu Asp Tyr Asn Arg Leu Arg Pro Leu Ser Tyr Arg Gly Ala
65 70 75

GAT GTG TTT TTG GCC TTT TCT CTT ATA AGC AAG GCC AGT TAT GAA 290
Asp Val Phe Leu Leu Ala Phe Ser Leu Ile Ser Lys Ala Ser Tyr Glu
80 85 90

AAC ATC TAC AAA AAG TGG ATC CCA GAG CTA AGA CAT TAT GCT CAT AAT 338
Asn Ile Tyr Lys Lys Trp Ile Pro Glu Leu Arg His Tyr Ala His Asn
95 100 105 110

GTA CCA GTT GTG CTT GTT GGA ACC AAA CTA GAT TTT CGA GAT GAC AAG 386
Val Pro Val Val Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Lys
115 120 125

CAG TTC CTC ATT GAT CAC CCT GGA GCA ACA CCA ATA TCA ACA TCT CAG 434
Gln Phe Leu Ile Asp His Pro Gly Ala Thr Pro Ile Ser Thr Ser Gln
130 135 140

FIGURE 4A



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GGA GAA GAA CTA AAG AAG ATG ATA GGA GCA GTT ACT TAT ATA GAA TGC 482
Gly Glu Glu Leu Lys Lys Met 150
Ile Gly Ala Val Thr Tyr Ile Glu Cys 155

AGC TCC AAA ACC CAA CAG AAT GTG AAG GCT GTT TTC GAT GCT GCA ATA 530
Ser Lys Thr Gln Gln Asn Val Lys Ala Val Phe Asp Ala Ala Ile 170
160 165

AAA GTA GCT TTG AGG CCA CCA AAA CCA AAG AGA AAG CCT TGC AAA AGG 578
Lys Val Ala Leu Arg Pro Lys Pro Lys Arg Lys Pro Cys Lys Arg 190
175 180 185

AGA ACA TGT GCT TTC CTT TGAATATTGG ATCATTTATTA CAGTCAAAAA 626
Arg Thr Cys Ala Phe Leu 195

CAGTTAACAA AAGCTGTTGC AGATAAACAC TGAATCTGCT ATAGTTTGTT TTTGGTTTAC 686

ATAATGTTCCA CGTGAAACTA TGAAGCATCT CTAAGAAAAAC CCAAACTATC ATATCAACCC 746

ATCGATCAAT GAATCGATTT CAATTTTTCGC AGTATAAGTT CCTTTTAAATC CTTTCTTTTT 806

ACTTCATTTT ATAACGAATT CTATGGATAA TGTTCCTTAC AAACATGTCA TTACAATGTT 866

TAATTATAAA TTCCATTCTT CTATTTTACT AAAAAAAAAA AAAA 910

FIGURE 4B



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20 40 60
TTGGATGAGA ACCAATTTT AATAGTAAAN CCTAACCAAT TTTTAATAAT AAAGCTGACT
80 100 120
CCTAGTACAA GAGCTTTTAT TCATTCTTCT ATTTTGCTTT CCTCTAGGCT TGGCAATCGA
140 160 180
GAATTTTCTT GTGTTACAAT ATAATAAATA CATCGTAGAA ATAAATTTTA TTCAAATTTGA
200 220 240
AGTCTTAACC ATCTTTAATA TTTGTAGATG TAATTTAAAT GAAAGATAAA TACATATTCT
260 280 300
TGGACATGTA TTTTCATCTT AATGTTTGTG GCTTTGGTGA TAGGTGTATT GATGTACGAT
320 340 360
GTCTTTTAAA TCACATATCA CATTTTGAGT TTGTATGATG ATAAAGTCGAC ATAANCGAAA
380 400 420
TATGGTGTGA TCCTTCACTTT TGAACCTTGA TAAAGTCACCA AACTTTAACA AAGTTTGATT
440 460 480
GTGTACATAT ATATATATAT CTTCAAAATT TATAATAAAA ATTGTGTTTA AATAATTTAC
500 520 540
AGTTATATTA TTTTATTATC TCTAAATTTA TTTGTGCGCA AATTTTTAGT TGATATTTTA
560 580 600
ACATAAAAAA AATTGTACAC ATTTACAAGC CCATATACAA ATAATTATAT AAATATTTCAT

FIGURE 5A

TAAAAAATAT	620	ATTTAAATAT	AGGATATAAA	TATAACTATT	TTAGAATTAT	TCTACTTTAA	660
GATAACATAG	680	GTAAAAATGTA	TAAATTAATAA	GGTTAGTTTA	TTGTAAAGAT	GAGTATATAT	720
GTCGTAAACA	740	TAATCACTAA	CCATTTTAT	TAACTTCTTG	GTTTGAAGT	TCCAAAAAGA	780
AAATGGAAGG	800	GAAATTTGAG	AGTAAAGTTCA	TGTTTATATT	ATACATAATG	AAGTTGATGT	840
TTTCCTCTTT	860	TAAATATTTT	TATACAAAAAT	ATTTAAATAA	AATAATTAAAG	GATTGAATGA	900
AAAAATATAAT	920	GAAAGTCGTT	TTACTAATAG	TCATATTGCA	TTTGTGCGCA	TCTACTTAAA	960
TAATAGATAA	980	ATTAATTGTG	GTACATTAGA	TCAAAGAACA	AACTAGATTT	TGTCCCATTC	1020
TATTGTAAA	1040	AGCTGGTCCG	TTTACATTAA	AATAAGGTAC	ATGTTACATG	CCACGTATAA	1080
CTATCTGGTT	1100	ATTCATATCAA	TCACGCTAAT	TTTTAACAGT	AGAAATGAAT	GTAATTTTAA	1140
AATAGAAAAGG	1160	GTCAAAATTGT	TATTTGATCT	AACACGTAGG	GATTAATTAA	CTTATTTTCC	1200

FIGURE 5B



08/984,099

TAAAGAAATA	1220	AATTGAATC	TTAATACAA	AACCTTCATG	ATACTTTTAT	1260
CATATTTTAC	1280	ATATTGTGAG	AGTAACAAAR	TTAAAAAACA	TAGAAACACC	1320
AAAAGTTAGT	1340	TATGGTGTGA	CTCATATACA	CAGTTAAAAAT	TTTGAATAAAAT	1380
GTCAITTAATT	1400	CCATCATGGG	TTTTTTTTTTT	TCTAGTTAAG	CCATAATTAT	1440
ATCATTAATC	1460	CTATCAATAC	CCCGCCCTGC	CTCCCTCCCT	CAATACTTAA	1500
CACCCAGCAC	1520	CAAACGCACT	TTAATAGCCA	CCTATTCTTA	GCCATGTCCT	1560
GAAAAGTAAA	1580	GCTAACCTGC	AATCATTCCA	TATCGAGGCC	TCAACAGATA	1620
ATGGGTTTGC	1640	ACCAAGTTGT	TAAAAACCCGG	CCCTCAACTT	CCCTTTTCTT	1680
CCACTCCACA	1700	CCCTCCAATT	TTCTTCATAT	GGTTCTFATTA	TAAGTTCTTT	1740
AATCAAGATA	1760	AGTCCCTCAGC	AAACAAAAAA	CCATGGCTCT	CGAGCAAGAT	1800

FIGURE 5C



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1820	1840	1860
CAGAGCTCTG AATATTGGAT CATTATTACA GTCAAAAACA GTTAACAAAA GCTGTTGCAG		
1880	1900	1920
ATAAACACTG AATCTGCTAT AGTTTGTGTTT TGGTTTACAT ATGTTCCACG TGAAACTATG	*	
1940	1960	1980
AAGCATCTCT AAGAAAACCC AAACATATCAT ATCAACCCAT CGATCAATGA ATCGATTTC		
2000	2020	2040
ATTTTCGCAG TATAAGTTCC TTTTAATCCT TTCCTTTTAC TTCATTTTAT AACGAAATCT	*	
2060	2080	2100
ATGGATAATG TTCCCTACAA ACATGTCATT ACAATGTTTA ATTATAAATT CCATTCCTCT		*
2120	2140	2160
ATTTTACTAA GATATTAGTA ACTTCAAACT GCTGATTTT ACTAATTTAT TATTTATAAA		
2180	2200	2220
TTGTTAGAAAT GATTATTTT CAATAATTTA ACAACAATAT TTAATATTAT TATTATTATT	*	
2240	2260	2280
ATTCTCAAT TTTTATTAAA CAAAAACATA AATTTTGAC AAATTAAAAA AAATGAAATTA		
2300	2320	2340
ATTCTCAAT TTTTCGTGCA ACTATTACAA AAATCCTTCA TAGTCCCTAAT CTTAATTGGA	*	
2360	2380	2400
TGCAGAGGTG ATAATAATCT TAATTGTATG CAGAGGTAAT AATGGGCCGG GTTTGAGCTG		*

FIGURE 5D

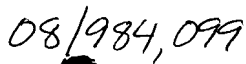


FIGURE 5E



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3020 ATGTACCGNT ATTATTTAT TTATTGAAAT TGGCATTATT TCTTG
3040

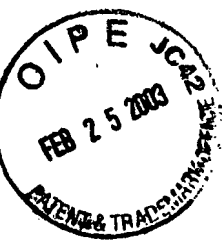
FIGURE 5F



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GGGCATTCCA CACGACCATG TGTCCTCCCTAT TTCCAGGCAT TTTGAGACTT CACCTAAACT 60
TCTAGAGTTG TTTCAAAATTA GCCCCTATTT GTTCTTAAAT CATTTAGGA TCTTGTAAC 120
TCGTATTAG GACTAAATGT GTAAATTTATA CTTTAATTAT GATTGATTAA TTGATTGATT 180
TNGTAGTAAT GCCCGTGACC CTAATCCGTT AGCGAAGAGG GGTAGGGGT TAGGGGTTTT 240
ATTATTATTT TTTAGATATT GTATAACTCT TGTTTTTATTT TTAAATTTTGT TACTATTCA 300
AAGGCATTTG TTTGTAGTGT TATTTCGAGT AGGTTTTATG GGTGAACAAC CCTTGACCGC 360
CAAATCAATC ACAAGAGTTC AACATTTTAT TTATTTTGAA ATGTATTAAA AATCGTTAAT 420
CTATATATTC GCCCCATTAT TGGGATTAAA TATTCACAAG GTTTAGACC GTCATGAGAC 480
AGATTAGTTT TATCTTACTG ATGGTCACAT CACAATAGTA ATTCAACTTA ATACGAGAGG 540
AACCATTGAT TCACGCAATT GGTCATCGCA CTTAGTTGAA AAGCTAGGGG TCGGAAGCTA 600
CCGTACGCTG GATTATGATT GAACACCTCT AAGTCAGAAT CCGAATTAGA AACAAATGCAC 660
GTGTCCGTTG CCTGATTGCC AACCCCAATA ACACGTGTTG TAGGTTTAAAC CATGTTTATG 720
AAAGATAAGG TTTTTTTTTT TATAAGCAAG CAACTATAGG GGTTTACTTC CGTGCGCAAA 780
TTTTTAGGTT ACCTATTTTG GGAGGGGGGA TTATGATTCA AGTGAAAGAA AGTTGGCACA 840
CACACAATCA GTACATCTGT TTGACAGAG ACACAGCCTA AAAACAGCAG CAAACAAGCC 900
TAAAGGAATC ACCCAAAAAC AACAAACCAA AGTACAGAGG AAAACAAGAG AATCCCTGTT 960
ACCACCAAGC TGAAAAAAG AAAATAAAAC TCAACTTTTG GCAATAAAAA CCCTCCTACC 1020
CTCAACCCCT AACACGCAA CAATCAGCAA TACTCCAAGC AACCATTTTC CTTACAAGTT 1080

FIGURE 7A



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TGTTTTTCTT GTGATTAAATC CAT ATG GCT AGC TCC ATG TCC CTT AAG CTT GCA 1133
Met Ala Ser Ser Met Ser Leu Lys Leu Ala>

TGT CTG CTA GTG TTG TGC ATG GTG GTG GGT GCA CCC CTG GCT CAA GGG 1181
Cys Leu Leu Val Leu Cys Met Val Val Gly Ala Pro Leu Ala Gln Gly>

GAC GTA ACC CGT GCT GAT GGC GTA GTC ACC CTT CCA CGC TGC CTT CCT 1229
Asp Val Thr Arg Ala Asp Gly Val Val Thr Leu Pro Arg Cys Leu Pro>

TTA TTG ATA GGG AAT GGT AAT GGT GCT GAT GCT GAT GTT GAT GCC CCA 1277
Leu Leu Ile Gly Asn Gly Asn Gly Ala Asp Val Asp Val Ala Pro>

GCT TGC TGC GAC ATC GTC AGG GGT CTC TTG AGC TCG CTG CTC TGT GGT 1325
Ala Cys Cys Asp Ile Val Arg Gly Leu Leu Ser Ser Leu Leu Cys Gly>

GGT GTT TAGGAACCG ATCTAGCTTG AAATCGGGTT CGGATACGGG TGGAGTTTCA 1380
Gly Val>

AATTGGTGTG TTATGGAATC CCAACTTAAT CGTGTTTAGG GGTGGGATCC AATGTGTGA 1440

TACATTACAG AGCATGGTTG TGGATTGTTT TCTCATATGT TTTGATTGAC TTGCTTGATA 1500

CATTGGATGA TTCGATAAAGG TGACCGGTTT ACCTGGGTAT CCAACCATCA TCCGATTACT 1560

TTTTAATAAT TATTGTGTTT TTCTTTATGT TGTCTGTCCT TTTGTTTCTT GATCTATAAC 1620

ATTATATTG CCCAAATTTT CGCATTTTCC ATATGTAGCT TATATATGTA TATATATATT 1680

CAATAAAGTA TATTGATTTA GCAGATGATT TGTGTATATA TTAAATCAA ATCAAACATT 1740

AATGATCATT CACTAGCGTC TTAATCTTGA AAAATTCATC AACGGTTATC CTTTGCAGCA 1800

TATATAAAAA AAATTGCCAA CCTATGCTT TTACACCTAA TTCAAGGGAT AACATAAGTC 1860

GATTAACG A 1871

FIGURE 7B



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Coker 130	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
1	80.35	.3206	0.3266	91.84	0.16	5.51	91.84	5.51	88.4
2	77.62	.3232	0.3282	90.6	0.66	6.45	90.6	6.48	84.2
3	80.98	.3197	0.3257	92.12	0.13	5.04	92.12	5.04	88.6
4	80.16	.3200	0.3255	91.75	0.35	5.00	91.75	5.01	86.1
5	77.03	.3220	0.3271	90.33	0.61	5.84	90.33	5.87	84.1
6	73.67	.3258	0.3293	88.76	1.35	7.14	88.76	7.26	79.4
7	82.43	.3178	0.3237	92.76	0.15	4.05	92.76	4.05	87.9
8	82.21	.3196	0.3255	92.66	0.19	4.99	92.66	4.99	87.9
9	81.19	.3194	0.3241	92.21	0.77	4.42	92.21	4.48	80.2
10	76.11	.3243	0.329	89.9	0.74	6.89	89.9	6.92	84
11	82.28	.3178	0.3236	92.69	0.19	4.00	92.69	4.00	87.3
TOTAL	874.03	3.5302	3.5883	1005.62	5.30	59.33	1005.62	59.61	938.10
MEAN	79.46	.3209	.3262	91.42	0.48	5.39	91.42	5.42	85.28
S.D.	2.91	.0026	.0020	1.33	0.38	1.08	1.33	1.11	3.22
RANGE	82.43-73.67	.3858-.3178	0.3293-.3236	92.76-88.76	1.35-.13	7.14-4.00	92.76-88.76	7.26-4.05	88.6-79.4
AVER DEV	2.44	.0021	.0017	1.11	0.31	0.88	1.11	0.90	2.64
Coker 130	Hunter L	Hunter a	Hunter B						
1	89.63	0.15	5.42						
2	88.10	0.66	6.27						
3	89.98	0.13	4.98						
4	89.53	0.36	4.94						
5	87.76	0.61	5.69						
6	85.83	1.35	6.85						
7	90.79	0.15	4.03						
8	90.67	0.19	4.95						
9	90.10	0.78	4.38						
10	87.23	0.75	6.65						
11	90.70	0.19	3.98						
TOTAL	980.32	5.32	58.14						
MEAN	89.12	0.48	5.29						
S.D.	1.65	0.39	0.99						
RANGE	90.79-85.83	1.35-.13	6.85-3.98						
AVER DEV	1.37	0.31	0.81						

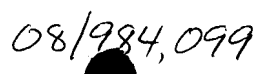
FIGURE 9

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5148	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
68-1	60.76	0.34	0.35	82.24	2.32	15.11	82.24	15.28	81.3
68-1	61.89	0.34	0.34	82.82	1.97	14.31	82.85	14.44	82.2
50-2-1	78.39	0.3324	0.3375	90.95	0.68	11.29	90.95	11.31	86.6
50-2-1									
(lint fiber)	21.49	.3155	0.3489	53.48	-8.01	7.97	53.48	11.29	135.2
5148	Hunter L	Hunter a	Hunter B						
68-1	77.94	2.25	13.35						
68-1	78.67	1.92	12.75						
50-2-1	88.53	0.69	10.71						
50-2-1									
(lint fiber)	46.35	-6.35	6.06						

FIGURE 10

[illegible]



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5616	Yxy, Y	Yxy, x	Yxy, y	Lab, L	Lab, a	Lab, b	LCh, L	LCh, C	LCh, h
11-1	72.26	0.3215	0.3254	88.09	1.1	5.06	88.09	5.17	77.8
11-2	58.69	0.3284	0.3335	81.12	0.6	8.36	81.12	8.38	85.9
11-2	52.78	0.3358	0.3335	77.74	3.55	9.22	77.74	9.87	69
11-1	72.03	0.3312	0.3338	87.98	1.72	9.52	87.98	9.67	79.8
11-1	72.34	0.3295	0.332	88.13	1.79	8.64	88.13	8.82	78.4
11-1	71.98	0.3295	0.3313	87.95	2.09	8.39	87.95	8.64	76.1
11-1	73.01	0.3256	0.3305	88.45	0.68	7.51	88.45	7.54	84.9
17-1-2	75.85	0.3274	0.3306	89.78	1.52	7.94	89.78	8.08	79.3
17-3-1	72.6	0.3271	0.3303	88.25	1.48	7.66	88.25	7.8	79.1
17-4-1	69.02	0.3352	0.3377	86.51	1.78	11.37	86.51	11.5	81.2
25-11-1	69.5	0.3364	0.3401	86.75	1.26	12.41	86.75	12.47	84.2
25-28-1	72.21	0.3324	0.3343	88.06	2.09	9.9	88.06	10.11	78.2
25-36-2	70.46	0.3327	0.3353	87.22	1.73	10.22	87.22	10.36	80.5
35-35-1	75.59	0.3268	0.3299	89.66	1.56	7.58	89.66	7.73	78.4
50-12-1	73.13	0.3284	0.3316	88.5	1.46	8.36	88.5	8.48	80.1
KS-11-2	65.33	0.3371	0.3388	84.65	2.07	11.83	84.65	12	80.1
5616	Hunter L	Hunter a	Hunter B						
11-1	85	1.09	4.89						
11-2	76.61	0.58	7.64						
11-2	72.64	3.38	8.22						
11-1	84.87	1.72	8.97						
11-1	85.05	1.79	8.2						
11-1	84.84	2.08	7.96						
11-1	85.44	0.67	7.18						
17-1-2	87.08	1.52	7.62						
17-3-1	85.2	1.48	7.31						
17-4-1	83.07	1.76	10.52						
25-11-1	83.36	1.25	11.43						
25-28-1	84.97	2.08	9.32						
25-36-2	83.94	1.72	9.56						
35-35-1	86.94	1.57	7.29						
50-12-1	85.51	1.46	7.96						
KS-11-2	80.82	2.04	10.81						

FIGURE 12

[illegible]